Mobilomic analysis suggests an important role of mobile genetic elements in bacterial adaptation towards pesticide degradation in on-farm biopurification systems

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Introduction

On-farm biopurification systems (BPS) are used to treat pesticide contaminated waste water. BPS receive pesticides at relatively high concentrations during a substantial time period of the year, thus perceiving strong and long-term selective pressures for evolution and growth of pesticide degrading bacteria. Plasmids and other mobile genetic elements (MGEs) collectively referred to as the mobilome, and in particular IncP-1 plasmids and IS*1071* elements, have been proposed to be important mediators in the genetic adaptation of bacteria towards pollutant biodegradation. This hypothesis was examined by a metagenomic exploration of the occurrence of IncP-1 and IS1071 elements as well as their accessory genes in BPS.

Objectives

Unravel the ecological significance of IS*1071* and IncP-1 as adaptive agents in bacterial communities of pesticide polluted environments.

Material & Methods

PCR and qPCR based detection of genetic markers for MGEs and catabolic genes were performed. Catabolic activities were examined by mineralization of ^{14}C-labbeled pesticides and degradation of chloroaromatic compounds. Longe range (LR) PCR methods directed toward amplification of accessory genes of IS*1071* composite transposons or IncP-1 plasmids were developed and performed on metagenomic DNA from microcosm BPS and BPS in operation. LR amplicons were sequenced using Illumina.

Results

High prevalence of as well IncP-1 plasmids as *IS1071* elements were observed in pesticide treated microcosm simulating the BPS filter matrix and in BPS in operation at farms, with concomitant increase in the catabolic capacity for pesticide and haloaromatic degradation and the in the abundance of catabolic genes compared to non-treated systems. The LR PCR approach generated amplicons up to 33kb, with detection limits of 10^5 copies per gram of soil. The method was successfully applied on DNA extracts from a microcosm BPS and a BPS in operation. Next generation sequencing of the amplified DNA revealed more than 350 kb of unique DNA that was highly enriched in coding sequences for organic xenobiotic catabolism including dioxygenases and dehalogenases.

Conclusion

Our data show the remarkable catabolic content of microbiota in a BPS at the genetic level and suggest that the mobilome is an important mediator in shaping this genetic content.